Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:06:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238641.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6238641 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238641.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:06:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238641.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,238,711
Mapped reads	13,618,052 / 89.36%
Unmapped reads	1,620,659 / 10.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	106,875 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	4,554,346 / 29.89%
Duplication rate	18.62%
Clipped reads	7,812,463 / 51.27%

2.2. ACGT Content

Number/percentage of A's	215,223,652 / 25.08%
Number/percentage of C's	155,726,876 / 18.15%
Number/percentage of T's	281,641,788 / 32.82%
Number/percentage of G's	205,431,378 / 23.94%
Number/percentage of N's	46,351 / 0.01%
GC Percentage	42.09%

2.3. Coverage

Mean	0.2773

Standard Deviation	2.7157

2.4. Mapping Quality

Mean Mapping Quality	41.47

2.5. Mismatches and indels

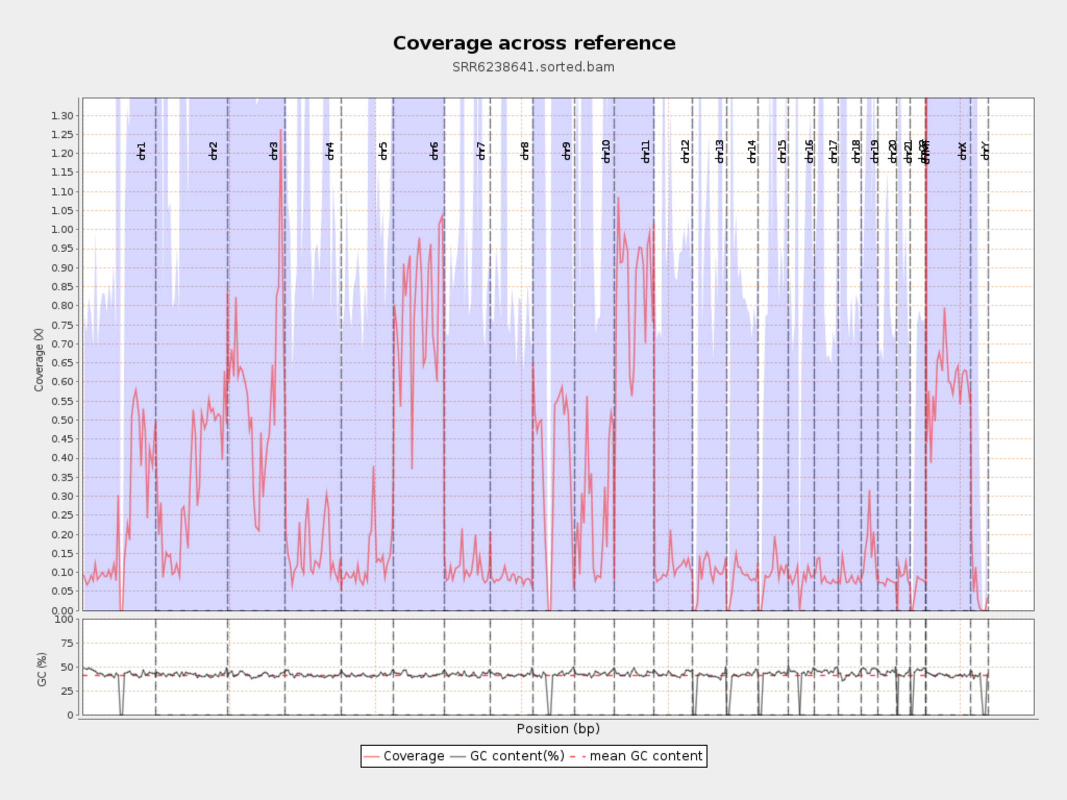
General error rate	0.53%
Mismatches	4,444,278
Insertions	53,706
Mapped reads with at least one insertion	0.39%
Deletions	203,336
Mapped reads with at least one deletion	1.48%
Homopolymer indels	43.02%

2.6. Chromosome stats

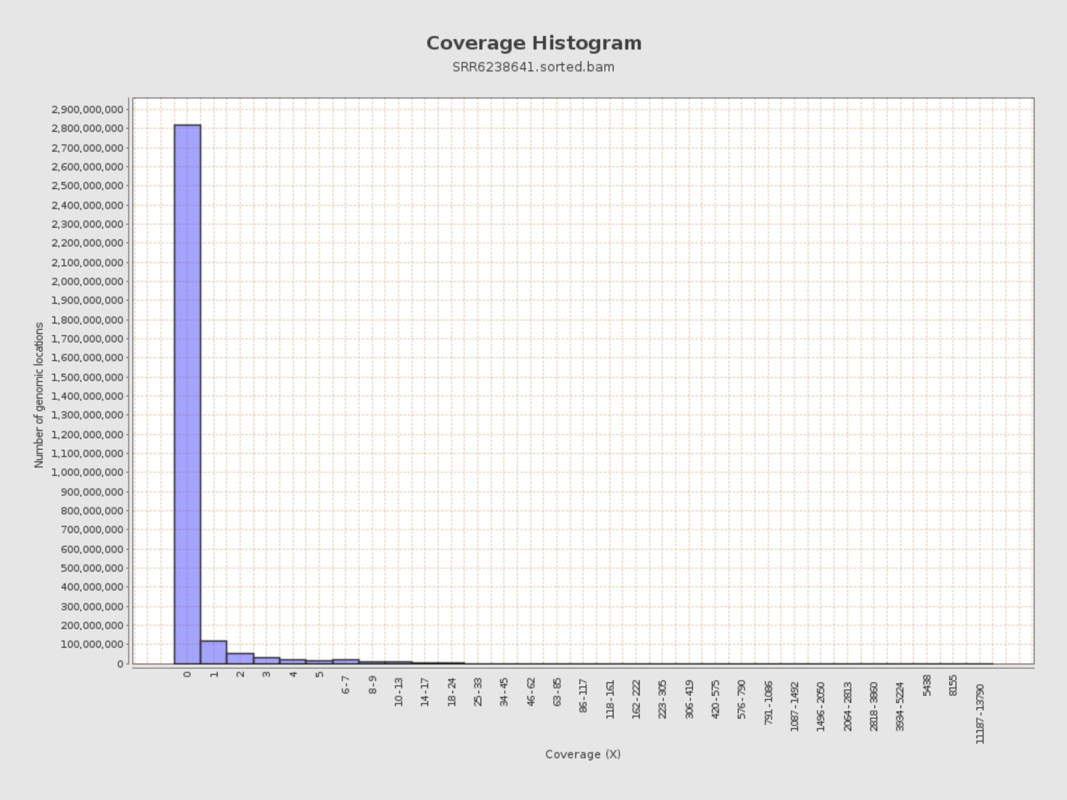
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	57134042	0.2292	3.8053
chr2	243199373	81379829	0.3346	6.1068
chr3	198022430	113697237	0.5742	1.9009
chr4	191154276	29127403	0.1524	1.1798
chr5	180915260	23615358	0.1305	0.9459
chr6	171115067	136207724	0.796	3.9943
chr7	159138663	17838511	0.1121	1.6825

chr8	146364022	12381648	0.0846	1.1722
chr9	141213431	54597169	0.3866	1.7296
chr10	135534747	35220788	0.2599	2.3802
chr11	135006516	113708683	0.8422	2.8767
chr12	133851895	15068048	0.1126	0.909
chr13	115169878	10828742	0.094	1.3791
chr14	107349540	8976143	0.0836	0.8101
chr15	102531392	9483192	0.0925	1.2325
chr16	90354753	7365467	0.0815	0.949
chr17	81195210	7281330	0.0897	1.0633
chr18	78077248	6809962	0.0872	3.7841
chr19	59128983	9704020	0.1641	2.4208
chr20	63025520	4701628	0.0746	0.7478
chr21	48129895	4298910	0.0893	1.0206
chr22	51304566	2975367	0.058	0.5654
chrMT	16571	303106	18.2914	12.5249
chrX	155270560	92902247	0.5983	2.2068
chrY	59373566	2816694	0.0474	1.1827

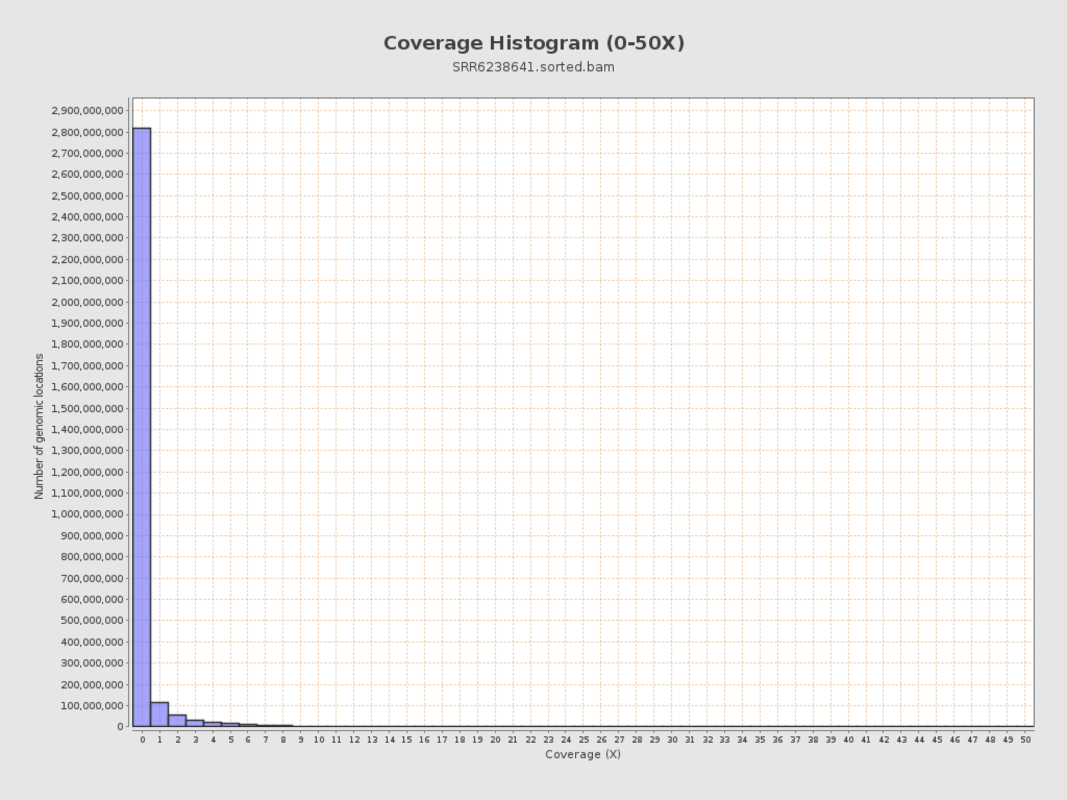
3. Results : Coverage across reference



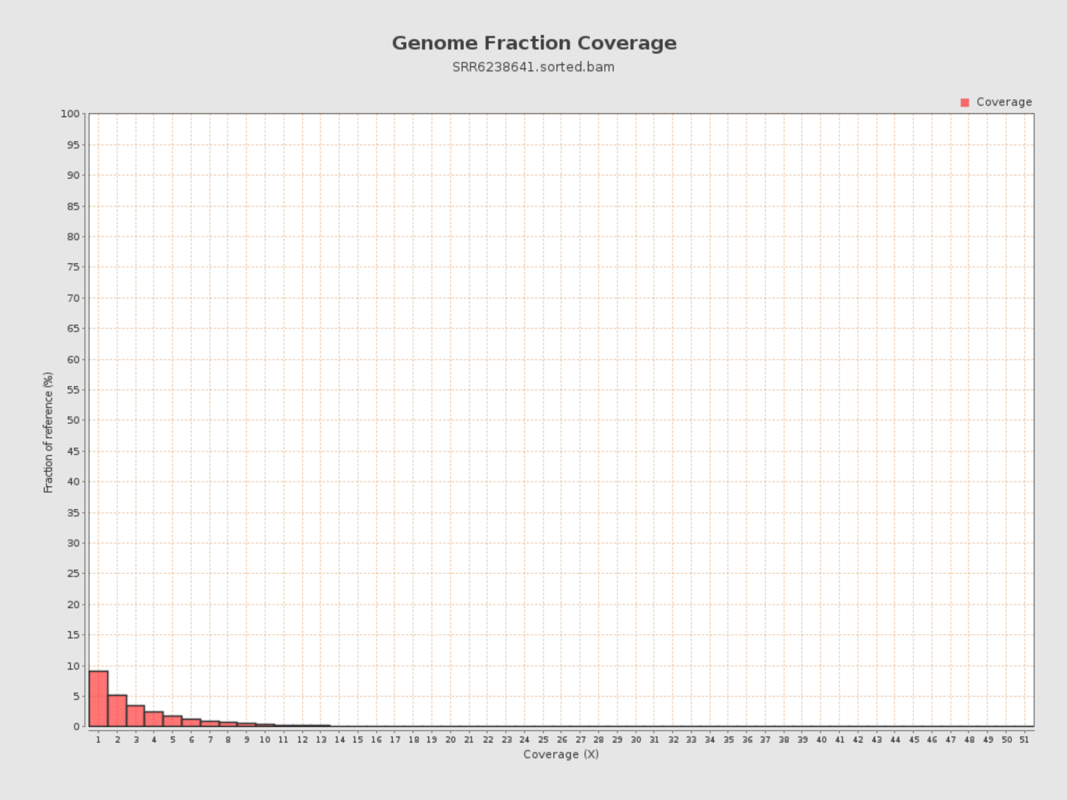
4. Results : Coverage Histogram



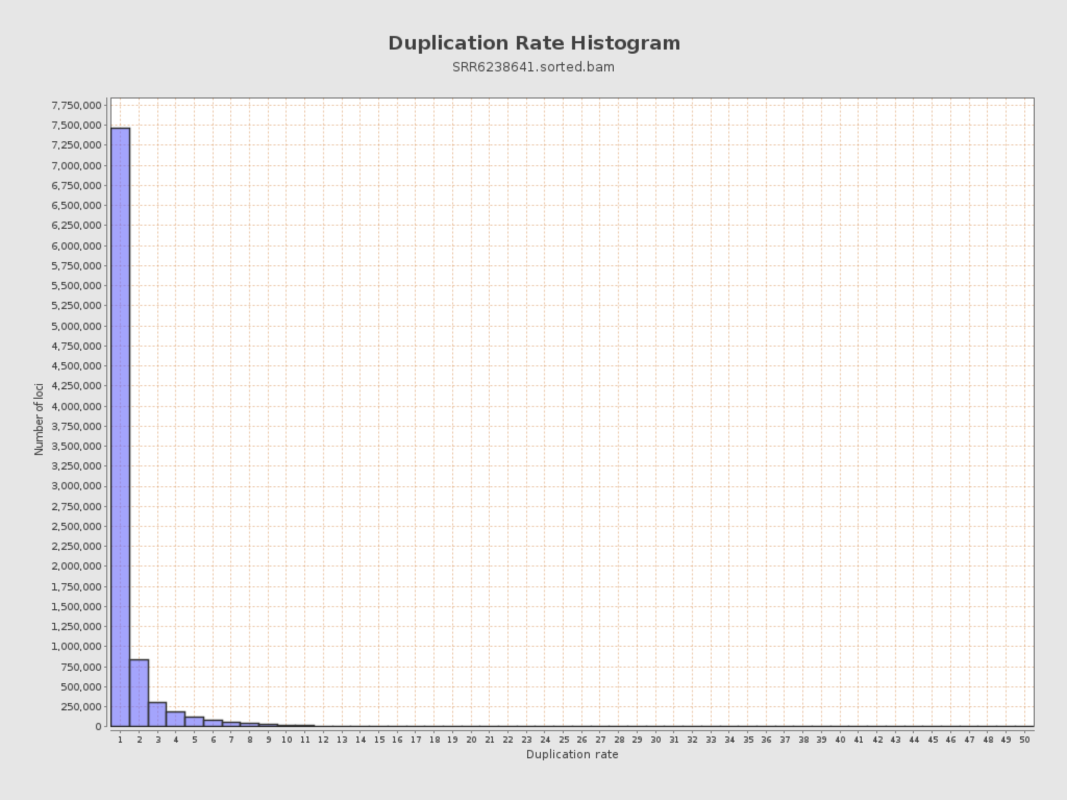
5. Results : Coverage Histogram (0-50X)



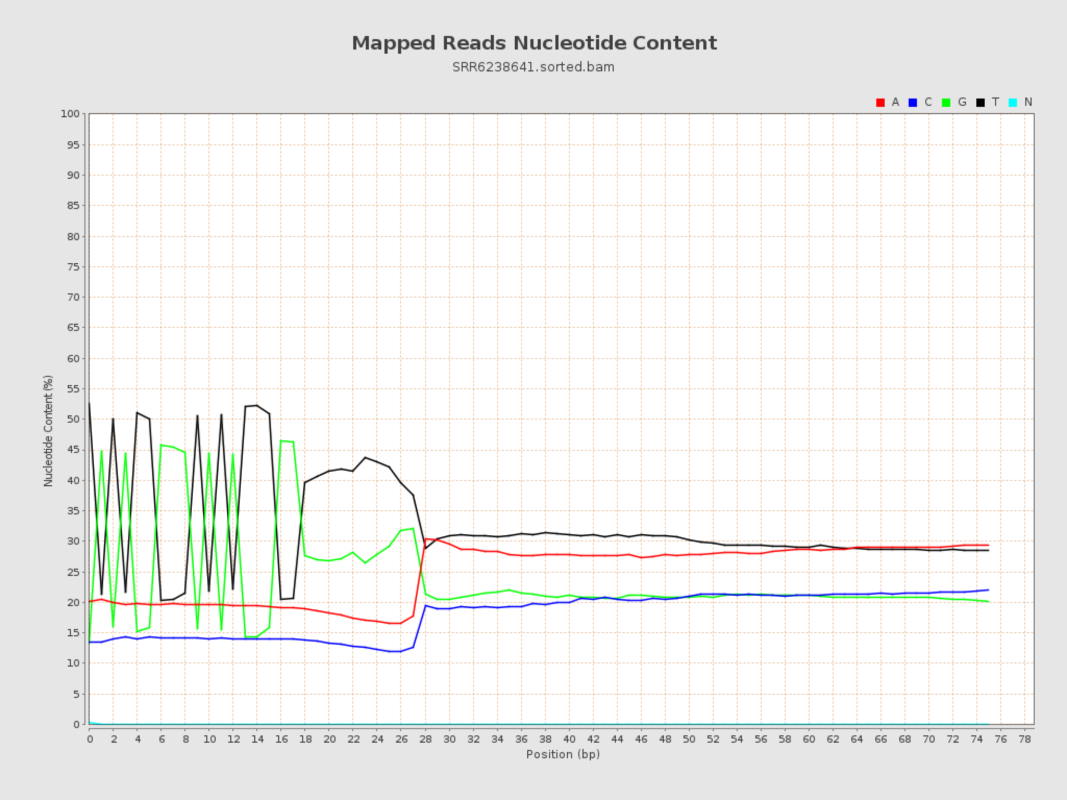
6. Results : Genome Fraction Coverage



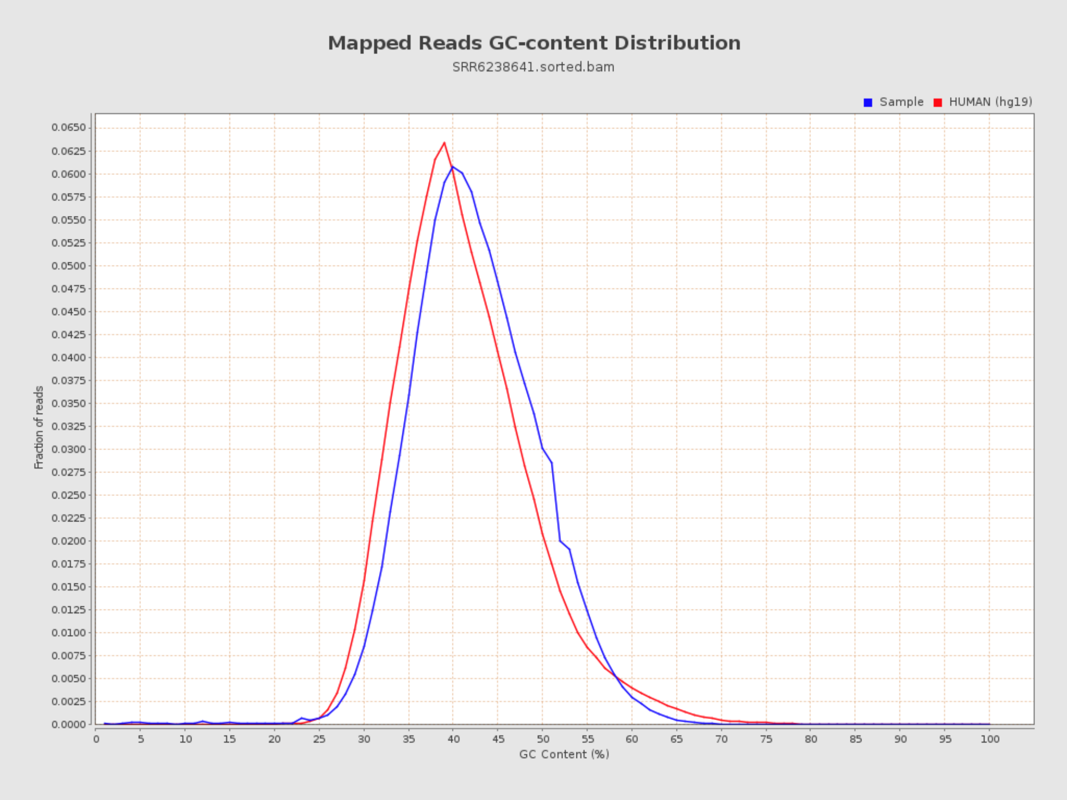
7. Results : Duplication Rate Histogram



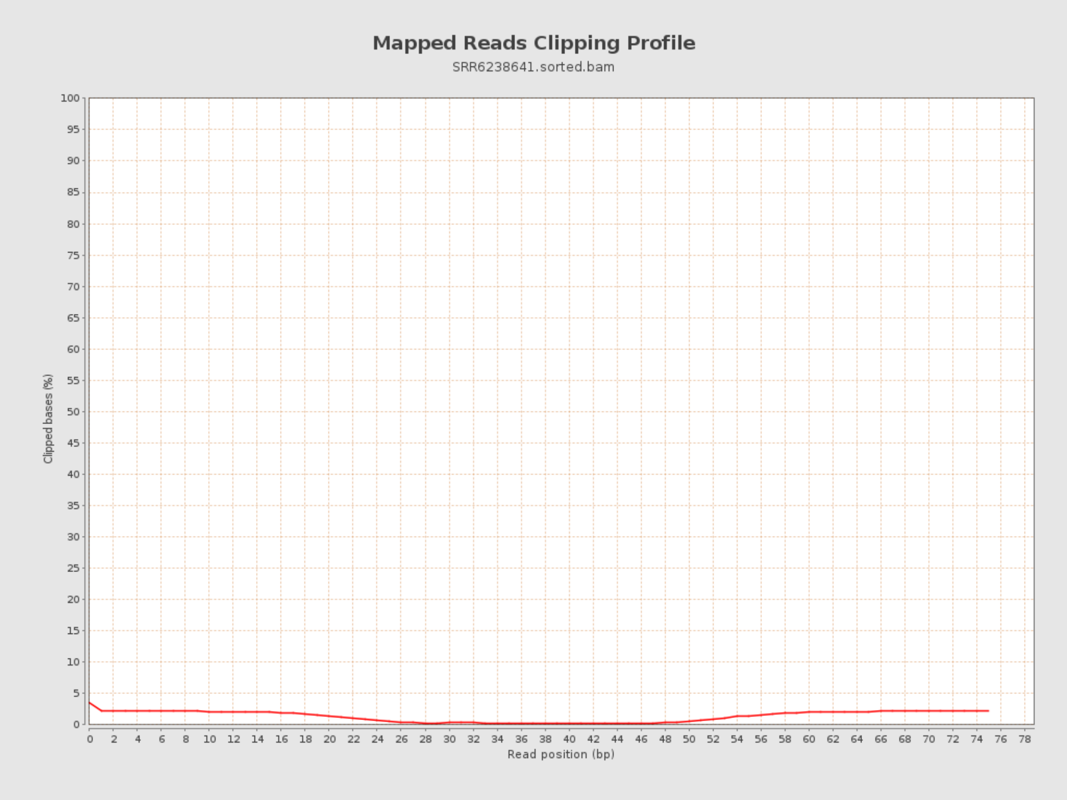
8. Results : Mapped Reads Nucleotide Content



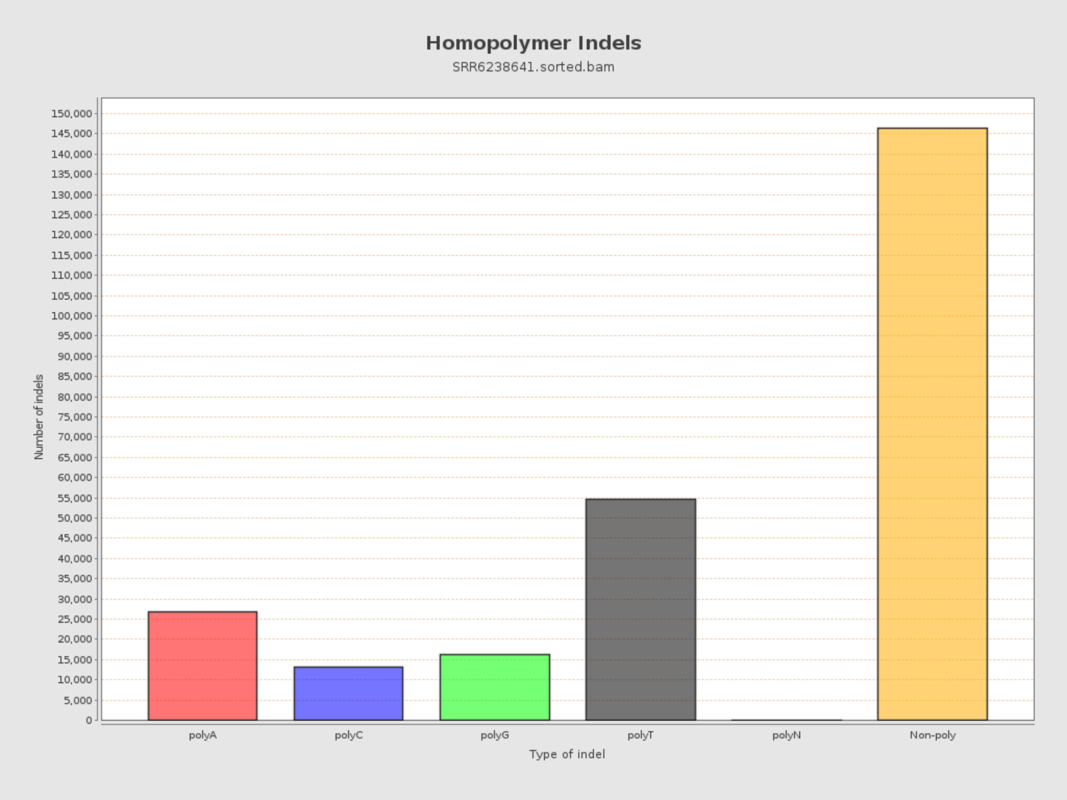
9. Results : Mapped Reads GC-content Distribution



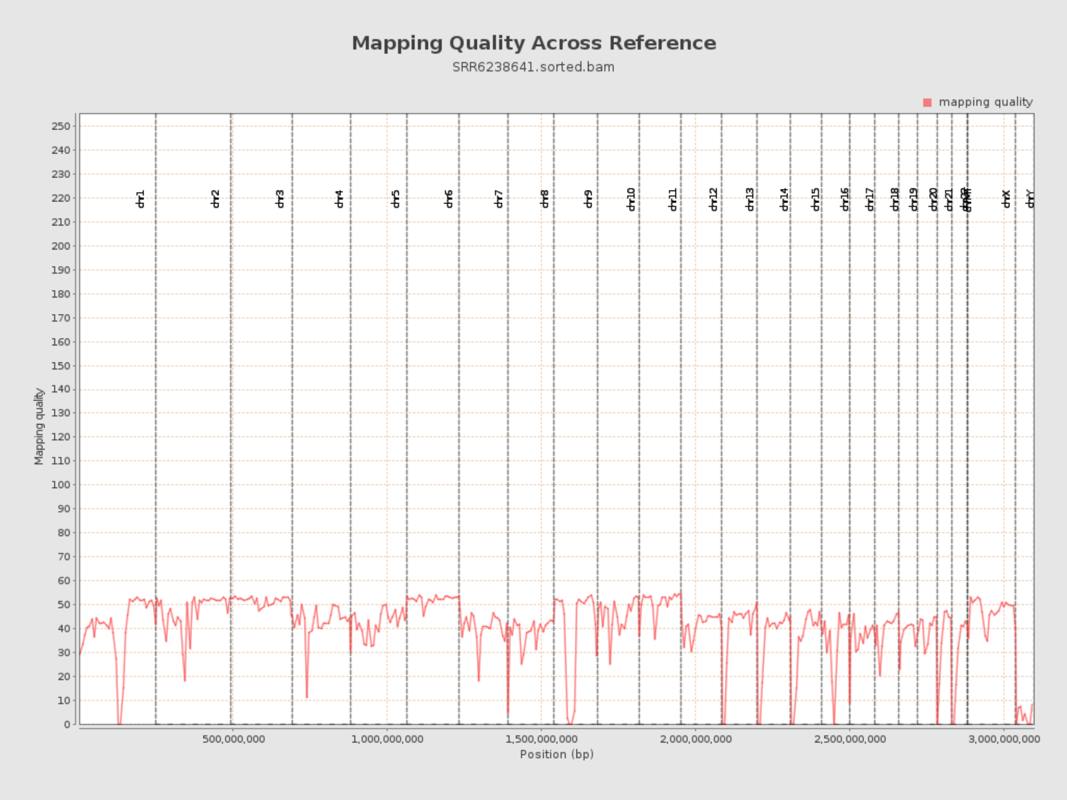
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram